

059  
16/9

#2

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/970,532

DATE: 11/20/2001

TIME: 09:54:16

Input Set : N:\Crf3\RULE60\09970532.txt

Output Set: N:\CRF3\11202001\I970532.raw

4 <110> APPLICANT: Taylor, J. Michael  
 5 Kehrli, Jr., Marcus  
 6 Lee, Eun-Kyung  
 7 Mwangi, Simon  
 9 <120> TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1  
 10 AND METHODS OF USE  
 12 <130> FILE REFERENCE: 08411-018001  
 14 <140> CURRENT APPLICATION NUMBER: 09/970,532  
 15 <141> CURRENT FILING DATE: 2001-10-03  
 17 <150> PRIOR APPLICATION NUMBER: 09/513,007  
 18 <151> PRIOR FILING DATE: 2000-02-25  
 20 <160> NUMBER OF SEQ ID NOS: 8  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 2440  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Bos taurus  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (294)...(1706)  
 33 <400> SEQUENCE: 1

34	tttttatttt tttttttctt ttttgggggg gaaaggggtg accccccttc cctcccacc	60
35	tcctctcagc tcaagttttc tcggagctct ccgggctctg ggccgcaggg ctggccttcc	120
36	gggttttgagg tcctccggat tgggctgtgt ccccgcccca gtctcaacc tccactcccc	180
37	gacccgaggg ccgggctcca ctgggcatac gcgaggaccg tgttgctgtc actgtcgcgg	240
38	gccgccactg ccccgacct gatgggggat tgagaggcca cagctggccg gac atg	296
39		Met
40		1
42	ggc ctc ccc acc gtg cct ggc ctg ctg ctg cca ctg gtg ctt cca gct	344
43	Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Pro Leu Val Leu Pro Ala	
44	5 10 15	
46	ctg ttg gca gat gtg tac ccc gca ggg gtt cag ggg ctg gtc cct cac	392
47	Leu Leu Ala Asp Val Tyr Pro Ala Gly Val Gln Gly Leu Val Pro His	
48	20 25 30	
50	ccc ggg gac ctg gag aag aga gag agt ccc tgt ccc caa gga aaa tat	440
51	Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro Gln Gly Lys Tyr	
52	35 40 45	
54	aac cac ccg caa aat agc acc att tgc tgc acc aag tgc cac aaa ggt	488
55	Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys Cys His Lys Gly	
56	50 55 60 65	
58	acc tat ctg tac aat gac tgt ccg ggt cca ggg cga gac acg gac tgc	536
59	Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg Asp Thr Asp Cys	
60	70 75 80	
62	agg gtg tgt gcc cct ggc acc tac act gcc ttg gag aac cat ctc aga	584
63	Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu Asn His Leu Arg	
64	85 90 95	
66	cga tgc ctg agc tgc tcc agg tgc ccg gac gaa atg ttc cag gtg gag	632

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67 Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met Phe Gln Val Glu
68      100      105      110
70 att tgc cct tgt gta gtg gac cgg gac act gtg tgc ggc tgc agg aag      680
71 Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys
72      115      120      125
74 aac cag tac cgg gaa tac tgg ggt gaa act ggc ttc cgg tgt ctg aac      728
75 Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe Arg Cys Leu Asn
76 130      135      140      145
78 tgc agc ctc tgt ccc aat ggc aca gtg aat atc ccc tgc cag gag aga      776
79 Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro Cys Gln Glu Arg
80      150      155      160
82 cag gac acc atc tgc cac tgc cat atg ggc ttc ttt ctt aaa ggc gcc      824
83 Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe Leu Lys Gly Ala
84      165      170      175
86 aag tgc atc tcc tgt cat gat tgt aag aac aag gag tgc gag aag tta      872
87 Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu Cys Glu Lys Leu
88      180      185      190
90 tgt cca acc cga cct tca act ggt aaa gac tct cag gac cca ggc act      920
91 Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln Asp Pro Gly Thr
92      195      200      205
94 aca gta cta tta ccc ctg gtg att gtc ttc ggg ctt tgc ctg gca tcc      968
95 Thr Val Leu Leu Pro Leu Val Ile Val Phe Gly Leu Cys Leu Ala Ser
96 210      215      220      225
98 ttc gcc tct gtc gtc tta gca tgt cgc tac cag cgg tgg aag ccc aag      1016
99 Phe Ala Ser Val Val Leu Ala Cys Arg Tyr Gln Arg Trp Lys Pro Lys
100      230      235      240
102 ctc tac tcc atc att tgc ggg cag tgc act ctg gta aaa gag ggg gag      1064
103 Leu Tyr Ser Ile Ile Cys Gly Gln Ser Thr Leu Val Lys Glu Gly Glu
104      245      250      255
106 cca gaa ctc ctg gtc ccg gcc cca ggc ttc aac ccc acc acc acc atc      1112
107 Pro Glu Leu Leu Val Pro Ala Pro Gly Phe Asn Pro Thr Thr Thr Ile
108      260      265      270
110 tgc ttc agc tcc acc cca agt tcc agt cct gtc tcc att ccc cct tac      1160
111 Cys Phe Ser Ser Thr Pro Ser Ser Pro Val Ser Ile Pro Pro Tyr
112      275      280      285
114 atc tcc tgt gac cgg tcc aac ttc gga gcc gtc gca tct ccc tcc agc      1208
115 Ile Ser Cys Asp Arg Ser Asn Phe Gly Ala Val Ala Ser Pro Ser Ser
116 290      295      300      305
118 gag acg gcc ccg ccc cat cta aag gct ggc ccc atc ctc ccg ggg cct      1256
119 Glu Thr Ala Pro Pro His Leu Lys Ala Gly Pro Ile Leu Pro Gly Pro
120      310      315      320
122 ccg gcc tcc acc cac ctc tgt acc ccg ggg cct ccg gcc tcc acc cac      1304
123 Pro Ala Ser Thr His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His
124      325      330      335
126 ctc tgt acc ccg ggg cct ccg gcc tcc acc cac ctc tgc acc cca gtt      1352
127 Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His Leu Cys Thr Pro Val
128      340      345      350
130 cag aag tgg gaa gcc agc gcc ccc agc gcc ccc gat cag ctc gcg gat      1400
131 Gln Lys Trp Glu Ala Ser Ala Pro Ser Ala Pro Asp Gln Leu Ala Asp

```

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```

132      355      360      365
134 gcc gac ccc gcg acc ctg tac gcg gtg gtg gac ggc gtg ccc ccg tcg      1448
135 Ala Asp Pro Ala Thr Leu Tyr Ala Val Val Asp Gly Val Pro Pro Ser
136 370      375      380      385
138 cgc tgg aag gag ttg gtg cgg cgg ctg gga ctg agc gag cac gag atc      1496
139 Arg Trp Lys Glu Leu Val Arg Arg Leu Gly Leu Ser Glu His Glu Ile
140      390      395      400
142 gag cgg ctg gag ctg gag aac ggg cgc cac ctg cgc gag gcg cag tac      1544
143 Glu Arg Leu Glu Leu Glu Asn Gly Arg His Leu Arg Glu Ala Gln Tyr
144      405      410      415
146 agc atg ctg gcg gcc tgg cgg cgg cgc acg ccg cgc cgc gag gcc acg      1592
147 Ser Met Leu Ala Ala Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
148      420      425      430
150 ctg gag ctg ctg ggc cgc gtg ctc agg gac atg gac ctg ctg ggt tgc      1640
151 Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
152      435      440      445
154 ctg gaa aac ata gag gag gcg ctg ggt ggc gcc gcc cgc ctc gcg tcc      1688
155 Leu Glu Asn Ile Glu Glu Ala Leu Gly Gly Ala Ala Arg Leu Ala Ser
156 450      455      460      465
158 gag ccc cgc ctt ctc tgg tgaagccccg cccctccgac tgcgggcctc      1736
159 Glu Pro Arg Leu Leu Trp
160      470
162 cccgcctcgc agacggctgc ttccttcctg tgccaggcag cccggaagga tctgcgagat      1796
163 gccctgtgga cctcctgttt tgttttgttt ttttctggag aggaagtctt ggaggagcag      1856
164 gcacgatctg gcagccactg acctggtgct actcactcag tgtacatagc ttttctcagc      1916
165 tgccctgagt tgtgtctgtg tgtagtgtgt gtctgcgtgc agtgcgtgtg tttgtgtctc      1976
166 tgtatgtgcg tctgtgtgat gtggagtgtg tgtactcgtg agagaggccg agtgtgcccg      2036
167 gagcccaagg cagtggttgc gaagatgagg ggcgcctgc cttattgcct gttttttggg      2096
168 cttggagaac tcagcaaggc gacttgggga acctacgtcg gtccctgagc cggtttcgca      2156
169 gtagataagc catctttgta tccactctgc acatccactc atccactctg tacactaata      2216
170 gaaactttgt tgccctgcct ggaccagctg aactgtcccc aggcagcggg ggagcacaga      2276
171 aaaatggggc ctcccaaggg agctagctgt tcagttcagt tcagtcgctc agtcgtgtcc      2336
172 gactctttgc gaccctgtga atcgaggga cttctgtaaa tacactaaaa tcttccaatt      2396
173 aaagctctgc cctggaggga ctggttaaaa aaaaaaaaaa aaaa      2440
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 471
177 <212> TYPE: PRT
178 <213> ORGANISM: Bos taurus
180 <400> SEQUENCE: 2
181 Met Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Pro Leu Val Leu Pro
182 1      5      10      15
183 Ala Leu Leu Ala Asp Val Tyr Pro Ala Gly Val Gln Gly Leu Val Pro
184      20      25      30
185 His Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro Gln Gly Lys
186      35      40      45
187 Tyr Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys Cys His Lys
188      50      55      60
189 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg Asp Thr Asp
190 65      70      75      80

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Output Set: N:\CRF3\11202001\I970532.raw

```

191 Cys Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu Asn His Leu
192      85                      90                      95
193 Arg Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met Phe Gln Val
194      100                      105                      110
195 Glu Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys Gly Cys Arg
196      115                      120                      125
197 Lys Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe Arg Cys Leu
198      130                      135                      140
199 Asn Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro Cys Gln Glu
200 145                      150                      155                      160
201 Arg Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe Leu Lys Gly
202      165                      170                      175
203 Ala Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu Cys Glu Lys
204      180                      185                      190
205 Leu Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln Asp Pro Gly
206      195                      200                      205
207 Thr Thr Val Leu Leu Pro Leu Val Ile Val Phe Gly Leu Cys Leu Ala
208      210                      215                      220
209 Ser Phe Ala Ser Val Val Leu Ala Cys Arg Tyr Gln Arg Trp Lys Pro
210 225                      230                      235                      240
211 Lys Leu Tyr Ser Ile Ile Cys Gly Gln Ser Thr Leu Val Lys Glu Gly
212      245                      250                      255
213 Glu Pro Glu Leu Leu Val Pro Ala Pro Gly Phe Asn Pro Thr Thr Thr
214      260                      265                      270
215 Ile Cys Phe Ser Ser Thr Pro Ser Ser Ser Pro Val Ser Ile Pro Pro
216      275                      280                      285
217 Tyr Ile Ser Cys Asp Arg Ser Asn Phe Gly Ala Val Ala Ser Pro Ser
218      290                      295                      300
219 Ser Glu Thr Ala Pro Pro His Leu Lys Ala Gly Pro Ile Leu Pro Gly
220 305                      310                      315                      320
221 Pro Pro Ala Ser Thr His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr
222      325                      330                      335
223 His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His Leu Cys Thr Pro
224      340                      345                      350
225 Val Gln Lys Trp Glu Ala Ser Ala Pro Ser Ala Pro Asp Gln Leu Ala
226      355                      360                      365
227 Asp Ala Asp Pro Ala Thr Leu Tyr Ala Val Val Asp Gly Val Pro Pro
228      370                      375                      380
229 Ser Arg Trp Lys Glu Leu Val Arg Arg Leu Gly Leu Ser Glu His Glu
230 385                      390                      395                      400
231 Ile Glu Arg Leu Glu Leu Glu Asn Gly Arg His Leu Arg Glu Ala Gln
232      405                      410                      415
233 Tyr Ser Met Leu Ala Ala Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
234      420                      425                      430
235 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
236      435                      440                      445
237 Cys Leu Glu Asn Ile Glu Glu Ala Leu Gly Gly Ala Ala Arg Leu Ala
238      450                      455                      460
239 Ser Glu Pro Arg Leu Leu Trp

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Input Set : N:\Crf3\RULE60\09970532.txt

Output Set: N:\CRF3\11202001\I970532.raw

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240 465                               470
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 543
244 <212> TYPE: DNA
245 <213> ORGANISM: Bos taurus
247 <220> FEATURE:
248 <221> NAME/KEY: CDS
249 <222> LOCATION: (1)...(543)
251 <400> SEQUENCE: 3
252 ctg gtc cct cac ccc ggg gac ctg gag aag aga gag agt ccc tgt ccc      48
253 Leu Val Pro His Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro
254 1                               5                               10                               15
256 caa gga aaa tat aac cac ccg caa aat agc acc att tgc tgc acc aag      96
257 Gln Gly Lys Tyr Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys
258                               20                               25                               30
260 tgc cac aaa ggt acc tat ctg tac aat gac tgt ccg ggt cca ggg cga      144
261 Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg
262                               35                               40                               45
264 gac acg gac tgc agg gtg tgt gcc cct ggc acc tac act gcc ttg gag      192
265 Asp Thr Asp Cys Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu
266                               50                               55                               60
268 aac cat ctc aga cga tgc ctg agc tgc tcc agg tgc cgg gac gaa atg      240
269 Asn His Leu Arg Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met
270 65                               70                               75                               80
272 ttc cag gtg gag att tcg cct tgt gta gtg gac cgg gac act gtg tgc      288
273 Phe Gln Val Glu Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys
274                               85                               90                               95
276 ggc tgc agg aag aac cag tac cgg gaa tac tgg ggt gaa act ggc ttc      336
277 Gly Cys Arg Lys Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe
278                               100                              105                              110
280 cgg tgt ctg aac tgc agc ctc tgt ccc aat ggc aca gtg aat atc ccc      384
281 Arg Cys Leu Asn Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro
282                               115                              120                              125
284 tgc cag gag aga cag gac acc atc tgc cac tgc cat atg ggc ttc ttt      432
285 Cys Gln Glu Arg Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe
286                               130                              135                              140
288 ctt aaa ggc gcc aag tgc atc tcc tgt cat gat tgt aag aac aag gag      480
289 Leu Lys Gly Ala Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu
290 145                              150                              155                              160
292 tgc gag aag tta tgt cca acc cga cct tca act ggt aaa gac tct cag      528
293 Cys Glu Lys Leu Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln
294                               165                              170                              175
296 gac cca ggc act aca                                                    543
297 Asp Pro Gly Thr Thr
298                               180
301 <210> SEQ ID NO: 4
302 <211> LENGTH: 181
303 <212> TYPE: PRT
304 <213> ORGANISM: Bos taurus

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/970,532

DATE: 11/20/2001

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Input Set : N:\Crf3\RULE60\09970532.txt

Output Set: N:\CRF3\11202001\I970532.raw